RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/202,5498
Source:	1600
Date Processed by STIC:	1/27/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- 3. Hand Carry directly to:
 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
 - U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09 202,5498				
ATTN: NEW RULES CASES	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE				
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."				
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.				
3Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.				
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.				
5_V Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.				
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has caused the <220> <223> section to be missing from amino acid sequences(s)				
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped				
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.				
8 Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000				
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.				
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence				
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)				
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.				
Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.				
	AMC/AGI. Biotochuslom Sustama Branch. 09/01/00/1				



1600

RAW SEQUENCE LISTING

DATE: 114. 19/2 ; Evers n p. 2

FATENT APPLICATION: US/09/202,549E TIME: 13:00:23

Input Set : A:\EP.txt

4 <110> AFPLICANT: Tsichlis, Philip Grimes, Leighton H

Output Set: N:\CRF4\01272003\I202549E.raw

```
% Zweidler-McKay, Patrick
      12 K1330 FILE REFERENCE: FCCC96-11
      5 .145
             CURRENT APPLICATION NUMBER: US 09/202,549E
     18 -141 - CURRENT FILING DATE: 1999-10-12
     19 -150 - PRIOR APPLICATION NUMBER: PC1/US97/10486
     2) -151 - PRICK FILING DATE: 1997-06-17
     23 - 150 - PRIOR APPLICATION NUMBER: US 66/019,808
     24 K151 - PRIOR FILING DATE: 1996-06-17
     PT 4160 - NUMBER OF SEQ 15 NOS: 70
     30 0170 - SÖFTWARE: Patentin version 3.1
     33 4210 - SEQ ID NO: 1
     34 :211 - LENGTH: 12
     31 M212 - TYPE: UNA
     36 <213 - DEGANTSM: Artificial Sequence
W--> 37 <220> FEATURE:
     35 PORTS OTHER INFORMATION: Gir-I binding sequence
W--> 39 <220> FEATURE:
     40 <03210 NAME/REY: misc feature
     42 (A23) WHEE INFORMATION: "n" is any nucleotide
W--> 44 <220> FEATURE:
     45 -0221: NAME, KEY: misc_feature
    46 + 0.220 + 1.00ATION: (9)...(9)
     47 -02230 OTHER INFORMATION: "n" is any nucleotide
    49 - (400) SEQUENCE: 1
W--> 50 naaatcacng ca
                                                                           12
     5: UNION SEQ II NO: 2
     54 K2110 LENGTH: 12
     BE KAND TYPE: DNA
     57 KD130 GRGANISM: Artificial Sequence
     5% <220. FEATURE:
     89 <223> OTHER INFORMATION: Gfi-1 binding sequence
W--> 60 <220> FEATURE:
     61 KANIS MIME/REY: SISS_iosture
     62 \times 2228 LOCATION: (9). \overline{1} ^{10}
     #3 *22 to OTHER INFORMATION: "n" is "t" or "a"
    ** *4" > JE, MENCE: /
W--> 66 taaatcacng ca
                                                                           12
    ···ij if, Hilbert
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1A1E: 1.17.1. + TIME: 1.1.1.1.1.1.
                       RAW SEQUENCE LISTING
                       FATENT ABELI ATI N: US/09/202,549E
                       Input Cet : A:\EP.txt
                        Title: N:\CRF4\01272003\I202549E.raw
      TI - VILS TYPE: INA
       L - 213 - WAWANISM: Artiff fiel Geguerre
       G COLOR FEATURE:
      Discuss other information: An expression regulatory in a segment
 W--> 76 <220> FEATURE:
      TT ×221 - NAME/KEY: misc feature
      78 ×222 · LOCATION: (1)...(1)
      73 <223 · OTHER INFORMATION: "n" is any nucleotide
W--> 81 <220> FEATURE:
      81 -221 - NAME/KFY: misc_feature
      83 H222 - LOCATION: (3)..(3)
      84 <223 · OTHER INFORMATION: "h" is any nucleotide
W--> 86 <220> FEATURE:
      87 K221 · NAME · KHY: misc feature
      88 < 3.32 + LOCATION: (4)..(5)
      89 KZ23 - OTHER INTOINMITION: "r" is "g" "c" or "t", or is absent, or is an Coligonuclectide
     90 two or more nucleotides
W--> 92 <220> FEATURE:
      98 <221 - NAME/KDY: misc_feature
      94 K222 - LOCATION: (6)..(6)
      91 <175 - C.HER INFORMATION: "n" is "a" "g" or "c", or is absent, or is an @ligonucleotide >
96 two or more nucleotides ;
W--> 98 <220> FEATURE:
      93 <221 NAME/KEY: misc feature
      100 < 32. > LOCATION: (9)..(9)
      131 (22) OTHER INFORMATION: "n" is "a" "g" or "c", or is absent, @r is an
Oligonucies de of the oligonucies de ser more nucleotides
      104 (4) : SEQUENCE: 3
W--> 105 nannnnacng ca
                                                                                     12
      108 -031 D SEQ ID NO: 4
      109 RE11: LENGTH: 24
      110 KB1. F TYPE: DNA
      111 KRID ORGANISM: Artificial Sequence
      113 <L200 FEATURE:
      114 (22) OTHER INFORMATION: Gfi-1 binding sequence
W--> 115 <220> FEATURE:
      116 KULL MAME/KEY: misc feature
      117 \pm 322: LOCATION: (2)...(2)
      116 <223. OTHER INFORMATION: ":" is "a" or "a"
W--> 121 <220> FEATURE:
      122 < 221; NAME/FEY: misc feature
      123 4722 \times 100ATION: (7)...(7)
      TN4 KDD3 / OTHER INFURMATION: "r" is "incsine" or "c"
W--> 126 <220> FEATURE:
      127 KL11> NAME/HEY: misc_feature
      135 + 2223  RECATION: (11) \overline{...} (15)
      124 - 129 - OTHER INFORMATION: "h" is "a" or "t"
      1 \times 1 \times 4^{\otimes}) \times JE, TEMTE: 4
W--> 132 anaaaanaaa tcacngcata tgcc
                                                                                     24
```

RAW SEQUENCE LISTING

FATENT AFELT WILL N: US/09/202,549E

Input Vet : A:\EP.txt
Outcur Vet: N:\CRF4\01272003\I202549E.raw

1.:	<pre>+COON BE; ID NOTE:</pre>	
1	+ 2014 (1FN9TH: 33	
• • • • • • • • • • • • • • • • • • • •	SIDS THE TUR	
· · ··	- 115 % GB/ ANISM: Artificial Copients	
	120 FEATURE:	
141	- 223 OTHER INFORMATION: Gii-1 bindin's sequence	
	<400 - SEQUENCE: 5	
144	appar dadra dataaatdad tgodtatoot gtig	33
147	<210 - SEQ ID NO: 6	
	<pre><'11 + LENGTH: }3</pre>	
	MAL - TYPE: CAN	
150	Kulo-ORBANISM: Artificial Sequence	
	km20 · FEATURE:	
153	4.123 - OTHER INFORMATION: Gfi-1 binding oligonucleotide	
155	GDE SEQUENCE: 6	
160	addatosbia bata:atham tghntathnt grg	3.5
	ART OF SECTION NO. 7	
	<pre><201 + LENGTH: 24</pre>	
161	ROLL - TYPE: DNA	
16.5	+313 + OFFANISM: Artificial Sequence	
	PRATTES:	
	(THER INFORMATION: Offi-1 binding cligonuclectide	
167	44: FEAUENCE: 7	
165	partheoatag athactgoot atoc	24
	+x10 + SEQ ID NO: 8	
17.5	THIL IBMSTE: 24	
	ALCHIYEE: DOWN	
174	UNIF OF MANISM: Artificial Sequence	
176	AND THE APPLIED.	
	RARE - CTHER INFORMATION: Gfi-1 binding oligonucleotide	
173	HOUSE SEQUENCE: 8	
	paphadataa otdaotgoot atoo	24
	ROJOU SEQ ID NO: 9	
	HOMMING DENGTH: 24	
	ROBERTYPE: DNA	
	HILLS OFGANISM: Artificial Sequence	
	KOLUGE FEATURE:	
	HOLLIN CTHER INFORMATION: Gfi-1 binding oligonucleotide	
	(400° SEQUENCE: 9	
	Dabbacataa ataactgsot atco	24
	<pre><10** 3EQ ID NO: 10</pre>	
196	KULID LENGTH: 24	
117	CHICA TYPE: DNA	
	40130 CRGANISM: Artificial Sequence	
	<220: FEATURE:	
	RADBH OTHER INFORMATION: Aft-1 birding bligarualcatida	
	of or Sequence: If	
25.4	naccadatáa átgaatanát ató:	2.4
201	Raisk arg id no: 11	

RAW SEQUENCE LISTING

FATENT AFENT WITTN: US/09/202,549E

Input Set : A:\EP.txt
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	11% LENGTH: L4						
	The Translation of the Control of th						
	while Chamilan Artificial deglence						
	%22°% FEATURE:	76. 4					
	<pre><223> OTHER INFORMATION: Gii-1 kindi</pre>	ng cliqu	nusiectide				
	<400% SEQUENCE: 11						
	cass.cataa atsasttost atss				2.4		
	<210 · SEQ IO NO: 12						
	k211 - LENGTH: 800						
	I KRIZ - TYPE: DNA						
	2 <213 · ORBANISM: Artificial Sequence						
	1330 · FEATURE:						
	<pre>3023 - OTHER INFORMATION: 3:1-1 bindi</pre>	ng seque	nice				
	400 - 3B2CEMOE: 12						
	woodwootyg styphogodd aauguddood hyg				60		
	Hodatagtaab godaatagyg potitionatt qab				120		
	intgoloaque dghigtacat caaqtqtato ata				180		
	unganggisa anggobogoo inggoartaig ood				240		
	intiquoagta pateraogta tragtoatoj sta				300		
	enat maatga gogtogaalay oggetetgant bab				3.60		
.:4:0	Hogt Haatigg gagittighth tightsaccacc and	aacagaa	Ctitccaaaa	tgtogtaada	$4 \stackrel{?}{\sim} 0$		
. : . : . :	Hotongoods attgabgsaa atgggoggta ggb	gtgt aug	guyggaggto	talataagda	480		
.144	paget botth laggidaacogt				500		
	HARD FOR ID NO: 13						
	+211 LENGTH: 800						
	HIZIZH TYPE: DNA						
145.3	-213 - CRMANISM: Artificial Seguence						
	-220 - FEATURE:						
25.3	+223 + CTHER INFORMATION: Gfi-1 pindi	ng seque	nce				
255	400 SEQUENCE: 13						
25.6	goodpotag otgadogodo aadgadoodo ogg	gattgac	gtcaataatg	acgtatgttc	60		
2.53	doatagtaac godaataggg actiticcati gab	gtcaatg	ggtggagtat	ttacggtaaa	120		
260	intgeneacti ggeagtaeat caagtgtate ata	tgccaag	tacgccccct	attgacgtca	180		
.1611	utganggtsa atggoodgoo tggoattatg ood	agtacat	gaccttatgg	gactttccta	240		
1111-1	stigocagia catolacgia tiagicalog cla	ttaccat	ggtgatgegg	ttttggcagt	300		
.1695	adathastgg gögtggatag oggittgadt dad	ggggagt	tocaagtoto	caccccattg	3.50		
263	acqtraatgg gagtttgttt tggcaccaaa ctc	aacggga	ctttccaaaa	tgtcgtaaca	420		
271)	actorgocco attyacquaa atgggoggta ggo	gtgtacg	gtgggaggtc	tatataagca	480		
2770	gaght ogtitt lagtgaabogt				500		
	K010 SEQ 10 NO: 14						
2., 6	4011 LENGTH: 500						
277	K212 - TYPE: DNA						
278	K213 - ORGANIŚM: Artificial Sequence						
	<pre><pre><pre><pre><pre><pre><pre><pre></pre></pre></pre></pre></pre></pre></pre></pre>						
. ~ 1	<pre>%238% OTHER INFORMATION: Off-1 bindi</pre>	ng segue:	nce				
	4460 SEQUENCE: 11	_					
	ignigostyg stydenyons aanganesse ngy	gattqa	ytcastasty	alatata**	t		
	rowiagtaán kinastágog antituratt gác				* * * *		
	ort a richartt og a ragt a ruf orakaat at at medite				1.45		
		•					

RAW SEQUENCE LISTING DATE: DATE: DATE: PATENT APPLICATION: US/09/202,549E TIME: DELETE: DEL

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190 atganggtað atggnuegsu týguáttatg nucagtabat gabottatgg gabtttþóta
297 migusagtā satstangtā thagtvanny mathabban ggtgatgogg thinggsagn
244 ahat aatigg griggetag nggtiinbasi nahqigaanti tobaagtoto babqirbattig
246 apgr aatgo badtitotti ripopaliyaa almaalgoga hiitirdaada toitib waada
Zir acto godoc attgacqoaa atgggdigta ggdgtgtacg gtgggaggto tatataaqca
                                                                         - : ⊱ ?
3)? gageregitt agtgaacegt
                                                                          5.00
303 4240 SER ID NO: 15
304 H211 - DENGTH: 12
305 H012 - TYPE: DNA
306 K. 13 · ORGANISM: Artificial Sequence
308 HUZU - FEATURE:
309 Wills OTHER INFORMATION: Gfi-1 binding sequence
311 -0400 - SERURNSE: 15
                                                                            12
51. Caara da as
315 -0004 - SEQ 00 NO: 16
PLANT SEMBRE
317 KOLO - TYPE: DNA
31c - COLD - OFGANISM: Artificial Sequence 30c - COLD - FEATURE:
3.15 -(400 - SEQUENCE: 16
GD: 'sathotgig to
                                                                            12
BUT HOLDER SECTION NO: 17
309 /211 - DENGTH: 12
3.54 P. II - TYPE: DNA
is - ... - OF AN SM: Artificial Sequence
SAR WINT & FEATURE:
$44 Add: THEF INFORMATION: Gfi-1 binding sequence
336 + 4:00 + SECURNOE: 17
337 yaaatcagtt aa
                                                                            12
340 A. 162 SEC II NO: 18
341 .111. LENGTH: 12
340 KUIDA TYRE: DNA
343 - Mills OF SANISM: Artificial Sequence
340 Hit by FEATURE:
347 HILES OTHER INFORMATION: Gfi-1 binding sequence
349 4400 F SEQUENCE: 18
310 maaatcagso ca
                                                                           12
SER ROTTO FEW ID NO: 19
3!4 <. 11: 1FNGTH: 12
35% -COLD TYPE: DNA
35% - LIE CRUANISM: Artificial Sequence
354 KIRCH FERTURE:
360 < 250 CIMER INFORMATION: Gfi-1 binding sequence
361 3400% SEQUENCE: 19
36 - graandagtt aa
344 P. 19 - SEQ ID NO: 20
367 - 1112 LENGIH: 12
368 <112> TYPE: DNA
```

RAW SEQUENCE LISTING ERROR SUMMARY

FATENT AFFLI MIL N: US/09/202,549E

Ingut Set : A:\EP.txt

Carry 3. Set: N:\CRF4\01272003\1202549E.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Fos. 1,9

Seq#:2; N Fcs. 9

Seq#:3; N Pos. 1,3,4,5,6,9

Seg#:4; N Fcs. 2,7,15

VERIFICATION SUMMARY

FATENT ARRITATION: US/09/202,549E TIME: 1:: 1::4

light Out : A:\EP.txt

purpor Vet: N:\CRF4\01272003\I202549E.raw

List Mist W: Missing Plank Line separator, <22.5 field identifier list M: ** W: Missing Plank Line separator, <10 - field identifier List M: **41 W: 40 "h" or "Maa" used, for JEC 10*:1 after p.s.: Lied M: **42 W: Missing Plank Line separator, <**20 - field identifier L: **76 M: **241 W: (46) "h" or "Maa" used, for SEC 10*:1 after pos.: L: 76 M: 243 W: Missing Plank Line separator, <220 - field identifier L: 105 M: 341 W: (46) "h" or "Maa" used, for SEC 10*:3 after pos.: C L: 115 M: 243 W: Missing Blank Line separator, <220 - field identifier L: 132 M: 241 W: (46) "h" or "Maa" used, for SEC 10*:4 after pos.: C L: 562 M: 243 W: Missing Blank Line separator, <220 - field identifier